

Amendments to the Specification:

Page 29, between lines 12 and 13, please insert the heading:

Brief Description of the Drawings

Page 53, amend the sentence at line 11 (paragraph [0212]) as follows:

[0212] Origin: online codon usage database ~~on www.kazusa.or.jp/codon~~

Page 56, line 20 to page 57, line 5 (paragraph [0229]), amend the paragraph as follows:

[0229] where <CU> represents the arithmetic mean of the relative adaptiveness values of the CDS codons, multiplied by 100, i.e. to represent the codon usage of a codon, for better comparability of the codon quality of different amino acids the codon which is best in each case for a particular amino acid is set equal to 100, and the worst codons are rescaled according to their tabulated percentage content. A CUScore of 100 therefore means that only codons optimal for the expression system are used. In the cytokine genes to be optimized, the CUScore was calculated on the basis of the codon frequencies in humans (Homo sapiens) which are listed in the table below. Only codons whose relative adaptiveness is greater than 0.6 are used in the optimizations. TABLE-

US-00008	AmAcid	Codon	Frequency
Ala	GCG	0.10	
	GCA	0.23	
	GCT	0.26	
GCC	0.40		
	Arg	AGG	0.20
		AGA	0.20
CGG		0.20	
CGA	0.11		
	CGT	0.06	
		CGC	0.19
Asn		AAT	0.45
	AAC	0.55	
		Asp	GAT
GAC			0.54
Cys	TGT		0.45
	TGC	0.55	
	End	TGA	0.61
TAG		0.17	
TAA		0.21	
Gln	CAG	0.73	
	CAA	0.27	
	Glu	GAG	0.58
GAA		0.42	
Gly		GGG	0.25
	GGA	0.25	
	GGT	0.16	

GCC 0.34 His CAT 0.41 CAC 0.59 Ile ATA 0.18 ATT 0.35 ATC 0.47 Leu TTG 0.12 TTA
0.08 CTG 0.38 CTA 0.09 CTT 0.13 CTC 0.20 Lys AAG 0.56 AAA 0.44 Met ATG 1.00
Phe TTT 0.45 TTC 0.55 Pro CCG 0.11 CCA 0.27 CCT 0.28 CCC 0.34 Ser AGT 0.15
AGC 0.24 TCG 0.05 TCA 0.15 TCT 0.18 TCC 0.22 Thr ACG 0.11 ACA 0.29 ACT 0.24
ACC 0.37 Trp TGG 1.00 Tyr TAT 0.44 TAC 0.56 Val GTG 0.45 GTA 0.12 GTT 0.18
GTC 0.24 Source: ~~GenBank~~ GENBANK™ release 138.0 [Oct. 15 2003] codon usage
database, ~~http://www.kazusa.or.jp/codon/~~